

RAW SEQUENCE LISTING

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Application Serial Number: 10/550, 934
Source: PCT
Date Processed by STIC: 10/07/2005

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/550,934

DATE: 10/07/2005
TIME: 10:11:24

Input Set : A:\14875-151US1.txt
Output Set: N:\CRF4\10072005\J550934.raw

3 <110> APPLICANT: Tsuchiya, Masayuki
 4 Kimura, Naoki
 5 Fukuda, Tatsuya
 7 <120> TITLE OF INVENTION: MODIFIED ANTIBODIES AGAINST CD22 AND USES THEREOF
 9 <130> FILE REFERENCE: 14875-151US1
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/550,934
 C--> 11 <141> CURRENT FILING DATE: 2005-09-28
 11 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/004696
 12 <151> PRIOR FILING DATE: 2004-03-31
 14 <150> PRIOR APPLICATION NUMBER: JP 2003-96950
 15 <151> PRIOR FILING DATE: 2003-03-31
 17 <160> NUMBER OF SEQ ID NOS: 36
 19 <170> SOFTWARE: PatentIn version 3.1
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 260
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Artificial
 26 <220> FEATURE:
 27 <223> OTHER INFORMATION: an artificially synthesized peptide sequence
 29 <400> SEQUENCE: 1
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 31 1 5 10 15
 33 Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Ala Glu Leu Ser Lys
 34 20 25 30
 36 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 37 35 40 45
 39 Thr Ser Tyr Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu
 40 50 55 60
 42 Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn
 43 65 70 75 80
 45 Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 46 85 90 95
 48 Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 49 100 105 110
 51 Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly
 52 115 120 125
 54 Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser Asp Ile Gln Leu
 55 130 135 140
 57 Thr Gln Ser Pro Ser Ser Leu Ala Val Ser Ala Gly Glu Asn Val Thr
 58 145 150 155 160
 60 Met Ser Cys Lys Ser Ser Gln Ser Val Leu Tyr Ser Ala Asn His Lys
 61 165 170 175
 63 Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu

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64	180	185	190	
66	Leu Ile Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe			
67	195	200	205	
69	Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Arg Val			
70	210	215	220	
72	Gln Val Glu Asp Leu Ala Ile Tyr Tyr Cys His Gln Tyr Leu Ser Ser			
73	225	230	235	240
75	Trp Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Asp Tyr Lys Asp			
76	245	250	255	
78	Asp Asp Asp Lys			
79	260			
82	<210> SEQ ID NO: 2			
83	<211> LENGTH: 810			
84	<212> TYPE: DNA			
85	<213> ORGANISM: Artificial			
87	<220> FEATURE:			
88	<223> OTHER INFORMATION: an artificially synthesized DNA sequence			
90	<220> FEATURE:			
91	<221> NAME/KEY: CDS			
92	<222> LOCATION: (14)..(799)			
95	<400> SEQUENCE: 2			
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97	Met Glu Arg His Trp Ile Phe Leu Phe Leu Phe Ser			
98	1 5 10			
100	gta act gca ggt gtc cac tcc cag gtc cag ctg cag gag tca ggg gct			97
101	Val Thr Ala Gly Val His Ser Gln Val Gln Leu Gln Glu Ser Gly Ala			
102	15 20 25			
104	gaa ctg tca aaa cct ggg gcc tca gtg aag atg tcc tgc aag gct tct			145
105	Glu Leu Ser Lys Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser			
106	30 35 40			
108	ggc tac acc ttt act agc tac tgg ctg cac tgg ata aaa cag agg cct			193
109	Gly Tyr Thr Phe Thr Ser Tyr Trp Leu His Trp Ile Lys Gln Arg Pro			
110	45 50 55 60			
112	gga cag ggt ctg gaa tgg att gga tac att aat cct agg aat gat tat			241
113	Gly Gln Gly Leu Glu Trp Ile Gly Tyr Ile Asn Pro Arg Asn Asp Tyr			
114	65 70 75			
116	act gag tac aat cag aac ttc aag gac aag gcc aca ttg act gca gac			289
117	Thr Glu Tyr Asn Gln Asn Phe Lys Asp Lys Ala Thr Leu Thr Ala Asp			
118	80 85 90			
120	aaa tcc tcc agc aca gcc tac atg caa ctg agc agc ctg aca tct gag			337
121	Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu			
122	95 100 105			
124	gac tct gca gtc tat tac tgt gca aga agg gat att act acg ttc tac			385
125	Asp Ser Ala Val Tyr Tyr Cys Ala Arg Arg Asp Ile Thr Thr Phe Tyr			
126	110 115 120			
128	tgg ggc caa ggc acc act ctc aca gtc tcc tcg ggt gga ggc ggt agc			433
129	Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Gly Gly Gly Ser			
130	125 130 135 140			
132	gac att cag ctg acc cag tct cca tca tct ctg gct gtg tct gca gga			481

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133	Asp	Ile	Gln	Leu	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ala	Val	Ser	Ala	Gly	
134				145					150						155		
136	gaa	aac	gtc	act	atg	agc	tgt	aag	tcc	agt	caa	agt	gtt	tta	tac	agt	529
137	Glu	Asn	Val	Thr	Met	Ser	Cys	Lys	Ser	Ser	Gln	Ser	Val	Leu	Tyr	Ser	
138				160					165						170		
140	gca	aat	cac	aag	aac	tac	ttg	gcc	tgg	tac	cag	cag	aaa	cca	ggg	cag	577
141	Ala	Asn	His	Lys	Asn	Tyr	Leu	Ala	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	
142				175					180						185		
144	tct	cct	aaa	ctg	ctg	atc	tac	tgg	gca	tcc	act	agg	gaa	tct	ggt	gtc	625
145	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	
146				190					195				200				
148	cct	gat	cgc	tcc	aca	ggc	agc	gga	tct	ggg	aca	gat	ttt	act	ctt	acc	673
149	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	
150	205				210					215					220		
152	atc	atc	aga	gta	caa	gtt	gaa	gac	ctg	gca	att	tat	tat	tgt	cac	caa	721
153	Ile	Ser	Arg	Val	Gln	Val	Glu	Asp	Leu	Ala	Ile	Tyr	Tyr	Cys	His	Gln	
154					225					230					235		
156	tac	ctc	tcc	tcg	tgg	acg	tcc	ggt	gga	ggg	acc	aag	ctg	gag	atc	aaa	769
157	Tyr	Leu	Ser	Ser	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	
158					240					245					250		
160	gac	tac	aag	gat	gac	gac	gat	aag	tga	taa	gcggccgcaa	t					810
161	Asp	Tyr	Lys	Asp	Asp	Asp	Asp	Lys									
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166	<211>	LENGTH:	262														
167	<212>	TYPE:	PRT														
168	<213>	ORGANISM:	Artificial														
170	<220>	FEATURE:															
171	<223>	OTHER INFORMATION:	an artificially synthesized peptide sequence														
173	<400>	SEQUENCE:	3														
174	Met	Asn	Phe	Gly	Leu	Arg	Leu	Ile	Phe	Leu	Val	Leu	Thr	Leu	Lys	Gly	
175	1				5					10					15		
177	Val	Lys	Cys	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Lys	
178					20					25					30		
180	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ala	Phe	
181					35					40					45		
183	Ser	Ile	Tyr	Asp	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	Glu	Lys	Arg	Leu	
184					50					55					60		
186	Glu	Trp	Val	Ala	Tyr	Ile	Ser	Ser	Gly	Gly	Gly	Thr	Thr	Tyr	Tyr	Pro	
187					65					70					75		80
189	Asp	Thr	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	
190						85					90					95	
192	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	Asp	Thr	Ala	Met	
193						100					105					110	
195	Tyr	Tyr	Cys	Ala	Arg	His	Ser	Gly	Tyr	Gly	Ser	Ser	Tyr	Gly	Val	Leu	
196					115					120					125		
198	Phe	Ala	Tyr	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	Ser	Ala	Gly	Gly	
199					130					135					140		
201	Gly	Gly	Ser	Asp	Ile	Gln	Met	Thr	Gln	Thr	Thr	Ser	Ser	Leu	Ser	Ala	

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202	145	150	155	160													
204	Ser	Leu	Gly	Asp	Arg	Val	Thr	Ile	Ser	Cys	Arg	Ala	Ser	Gln	Asp	Ile	
205					165				170						175		
207	Ser	Asn	Tyr	Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Asp	Gly	Thr	Val	Lys	
208						180			185						190		
210	Leu	Leu	Ile	Tyr	Tyr	Thr	Ser	Ile	Leu	His	Ser	Gly	Val	Pro	Ser	Lys	
211						195			200						205		
213	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Tyr	Ser	Leu	Thr	Ile	Ser	Asn	
214						210			215						220		
216	Leu	Glu	Gln	Glu	Asp	Phe	Ala	Thr	Tyr	Phe	Cys	Gln	Gln	Gly	Asn	Thr	
217	225					230				235						240	
219	Leu	Pro	Trp	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys	Asp	Tyr	
220						245				250						255	
222	Lys	Asp	Asp	Asp	Asp	Lys											
223						260											
226	<210>	SEQ	ID	NO:	4												
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228	<212>	TYPE:	DNA														
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232	<223>	OTHER INFORMATION:	an artificially synthesized DNA sequence														
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241																	
242					Met	Asn	Phe	Gly	Leu	Arg	Leu	Ile	Phe	Leu	Val	Leu	
					1				5						10		
244	act	tta	aaa	ggg	gtg	aag	tgt	gaa	gtg	cag	ctg	gtg	gag	tct	ggg	gga	
245																	
246	Thr	Leu	Lys	Gly	Val	Lys	Cys	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	
	15				20					25							
248	ggc	tta	gtg	aag	cct	gga	ggg	tcc	ctg	aaa	ctc	tcc	tgt	gca	gcc	tct	
249																	
250	Gly	Leu	Val	Lys	Pro	Gly	Gly	Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	
	30				35					40							
252	gga	ttc	gct	ttc	agt	atc	tat	gac	atg	tct	tgg	gtt	cgc	cag	act	ccg	
253																	
254	Gly	Phe	Ala	Phe	Ser	Ile	Tyr	Asp	Met	Ser	Trp	Val	Arg	Gln	Thr	Pro	
	45				50					55					60		
256	gag	aag	agg	ctg	gag	tgg	gtc	gca	tac	att	agt	agt	ggt	ggt	acc		
257																	
258	Glu	Lys	Arg	Leu	Glu	Trp	Val	Ala	Tyr	Ile	Ser	Ser	Gly	Gly	Thr		
	65				70					75							
260	acc	tac	tat	cca	gac	act	gtg	aag	ggc	cga	ttc	acc	atc	tcc	aga	gac	
261																	
262	Thr	Tyr	Tyr	Pro	Asp	Thr	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	
	80				85					90							
264	aat	gcc	aag	aac	acc	ctg	tac	ctg	caa	atg	agc	agt	ctg	aag	tct	gag	
265																	
266	Asn	Ala	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Ser	Ser	Leu	Lys	Ser	Glu	
	95				100					105							
268	gac	aca	gcc	atg	tat	tac	tgt	gca	aga	cat	agt	ggc	tac	ggt	agt	agc	
269																	
270	Asp	Thr	Ala	Met	Tyr	Tyr	Cys	Ala	Arg	His	Ser	Gly	Tyr	Gly	Ser	Ser	
	110				115					120							

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272 tac ggg gtt ttg ttt gct tac tgg ggc caa ggg act ctg gtc act gtc	433
273 Tyr Gly Val Leu Phe Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val	
274 125 130 135 140	
276 tct gca ggt gga ggc ggt agc gat atc cag atg acc cag act aca tcc	481
277 Ser Ala Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Thr Thr Ser	
278 145 150 155	
280 tcc ctg tct gcc tct ctg gga gac aga gtc acc att agt tgc agg gca	529
281 Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys Arg Ala	
282 160 165 170	
284 agt cag gac att agc aat tat tta aac tgg tat cag cag aaa cca gat	577
285 Ser Gln Asp Ile Ser Asn Tyr Leu Asn Trp Tyr Gln Gln Lys Pro Asp	
286 175 180 185	
288 gga act gtt aaa ctc ctg atc tac tac aca tca ata tta cac tca gga	625
289 Gly Thr Val Lys Leu Leu Ile Tyr Tyr Ser Ile Leu His Ser Gly	
290 190 195 200	
292 gtc cca tca aag ttc agt ggc agt ggg tct gga aca gat tat tct ctc	673
293 Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Ser Leu	
294 205 210 215 220	
296 acc att agc aac ctg gag caa gaa gat ttt gcc act tac ttt tgc caa	721
297 Thr Ile Ser Asn Leu Glu Gln Glu Asp Phe Ala Thr Tyr Phe Cys Gln	
298 225 230 235	
300 cag ggt aat acg ctt ccg tgg acg ttc ggt gga ggc acc aag ctg gaa	769
301 Gln Gly Asn Thr Leu Pro Trp Thr Phe Gly Gly Thr Lys Leu Glu	
302 240 245 250	
304 atc aaa gac tac aag gat gac gac gat aag tga taa gcggccgcaa t	816
305 Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys	
306 255 260	
310 <210> SEQ ID NO: 5	
311 <211> LENGTH: 116	
312 <212> TYPE: PRT	
313 <213> ORGANISM: Artificial	
315 <220> FEATURE:	
316 <223> OTHER INFORMATION: an artificially synthesized peptide sequence	
318 <400> SEQUENCE: 5	
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320 1 5 10 15	
322 Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser Tyr	
323 20 25 30	
325 Trp Leu His Trp Ile Lys Gln Arg Pro Gly Gln Gly Leu Glu Trp Ile	
326 35 40 45	
328 Gly Tyr Ile Asn Pro Arg Asn Asp Tyr Thr Glu Tyr Asn Gln Asn Phe	
329 50 55 60	
331 Lys Asp Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr	
332 65 70 75 80	
334 Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Tyr Cys	
335 85 90 95	
337 Ala Arg Arg Asp Ile Thr Thr Phe Tyr Trp Gly Gln Gly Thr Thr Leu	
338 100 105 110	
340 Thr Val Ser Ser	

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27
Seq#:28,29,30,31,32,33,34,35,36

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L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date